L Number	Hits	Search Text	DB	Time stamp
1	3	high-throughput same protein same microarray same (BSA or bovine serum albumin)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/07/31 09:58
2	3	(("6103479") or ("6548263") or ("20020103338")).PN.	USPAT; US-PGPUB; EPO	2003/07/31 10:26
4	0	aldehyde near3 treat same slide same amine	USPAT; US-PGPUB; EPO; DERWENT	2003/07/31 10:27
3	6	aldehyde near3 treated same slide same amine	USPAT; US-PGPUB; EPO; DERWENT	2003/07/31 10:28

throughput(P)(microarray or screening)(P)(spot or well or dot)(P)cm2

```
  research.  Use for software development or design or implementation
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  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 09:43:43 ON 31 JUL 2003

=> file .chemistry
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

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FILE 'USPATFULL' ENTERED AT 09:43:53 ON 31 JUL 2003
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=> throughput(P)(microarray or screening)(P)(spot or well or dot)(P)cm2
L1            1 FILE CAPLUS
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'DOT)(P)CM2'
L2            0 FILE BIOTECHNO
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'DOT)(P)CM2'
L3            1 FILE COMPENDEX
L4            0 FILE ANABSTR
L5            0 FILE CERAB
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'DOT)(P)CM2'
L6            0 FILE METADEX
L7            0 FILE USPATFULL
```

TOTAL FOR ALL FILES
L8 2 THROUGHPUT(P)(MICROARRAY OR SCREENING)(P)(SPOT OR WELL OR DOT)(P) CM2

=> d l8 ibib abs total

L8 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2002:662215 CAPLUS
DOCUMENT NUMBER: 138:90052
TITLE: Individually addressable parallel peptide synthesis on microchips
AUTHOR(S): Pellois, Jean Philippe; Zhou, Xiaochuan; Srivannavit, Onnop; Zhou, Tiecheng; Gulari, Erdogan; Gao, Xiaolian
CORPORATE SOURCE: Department of Chemistry, University of Houston, Houston, TX, 77004-5003., USA
SOURCE: Nature Biotechnology (2002), 20(9), 922-926
CODEN: NABIF9; ISSN: 1087-0156
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Miniaturized, spatially addressable microchips of peptides and peptidomimetics are powerful tools for high-**throughput** biomedical and pharmaceutical research and the advancement of proteomics. Here we report an efficient and flexible method for the parallel synthesis of peptides on individually addressable microchips, using digital photolithog. and photogenerated acid in the deprotection step. We demonstrate that we are able to synthesize thousands of peptides in a 1 **cm2** area on a microchip using 20 natural amino acids as **well** as synthetic amino acid analogs, with high stepwise yields and short reaction-cycle times. Epitope **screening** expts. using a p53 antibody (PAb240) produced clearly defined binding patterns. The peptidomimetic sequences on the microchip show specific antibody binding and provide insights into the mol. details responsible for specificity of epitope binding. Our approach requires just a conventional synthesizer and a computer-controllable optical module, thereby allowing potential development of peptide microchips for various pharmaceutical and proteomic applications in routine research labs.
REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 2 COMPENDEX COPYRIGHT 2003 EEI on STN
ACCESSION NUMBER: 2003(2):2903 COMPENDEX
TITLE: High **throughput screening** using enzyme assay **microarrays**.
AUTHOR: Gosalia, D.N. (Department of Bioengineering University of Pennsylvania, Philadelphia, PA, United States); Diamond, S.L.
MEETING TITLE: Proceedings of the 2002 IEEE Engineering in Medicine and Biology 24th Annual Conference and the 2002 Fall Meeting of the Biomedical Engineering Society (BMES / EMBS).
MEETING LOCATION: Houston, TX, United States
MEETING DATE: 23 Oct 2002-26 Oct 2002
SOURCE: Annual International Conference of the IEEE Engineering in Medicine and Biology - Proceedings v 2 2002.p 1628-1629, (IEEE cat n 02ch37392)
CODEN: CEMBAD ISSN: 0589-1019
PUBLICATION YEAR: 2002
MEETING NUMBER: 60461
DOCUMENT TYPE: Conference Article
TREATMENT CODE: Theoretical; Experimental
LANGUAGE: English
AN 2003(2):2903 COMPENDEX

AB We report a new slide based **microarray** platform for assaying multiple enzyme activities using fluorogenic substrates. The method enables us to achieve the microfluidic requirements for rapid reaction assembly and compartmentalization. We can thus determine enzymatic activities in individually controlled reaction environments containing cofactors, inhibitors and activators. Fluorogenic substrates in glycerol were arrayed onto glass slides with reaction volumes < 5 nL and feature sizes of <150mum. Our method allowed rapid multiple sample deliveries onto the slide (<3nL/**spot**) with no cross contamination between array positions. It enabled us to detect the activation of the fibrinolytic and coagulation proteases namely, thrombin, plasmin, factor Xa, tPa and kallikrein in human plasma. Enzyme - substrate - inhibitor assays using ten caspases were also performed. With over 400 **spots/ cm2**, combinatorial substrate libraries with different proteases can now be rapidly profiled. An assay to detect the dose response of a thrombin inhibitor benzamidine was performed. The inhibitor was arrayed in replicates onto selected positions on the chip. After sequential subnanoliter delivery of the reaction components, the result from the array was analyzed. The expected dose response from benzamidine was seen. A CV of 5.26% was achieved for 232 positions on the array not spiked with the inhibitor. Thus, with potentially several thousand compounds per slide, using rapid sub - nanoliter delivery of components and standard equipment, the true potential of the method is in the field of high **throughput screening**. 14 Refs.

```
=> file .jacob
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      24.93      25.14

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                         ENTRY    SESSION
CA SUBSCRIBER PRICE                                      -0.65      -0.65

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=> throughput(P)(microarray or screening)(P)(spot or well or dot)(P)(per cm)_
MISSING OPERATOR CM)_
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> throughput(P)(microarray or screening)(P)(spot or well or dot)(P)(per cm)
L9            0 FILE CAPLUS
L10           0 FILE BIOSIS
L11           0 FILE MEDLINE
L12           0 FILE EMBASE
L13           2 FILE USPATFULL

TOTAL FOR ALL FILES
```

L14 2 THROUGHPUT(P)(MICROARRAY OR SCREENING)(P)(SPOT OR WELL OR DOT)(P)(PER CM)

=> d l14 ibib abs total

L14 ANSWER 1 OF 2 USPATFULL on STN

ACCESSION NUMBER:	2003:3481 USPATFULL
TITLE:	Therapeutic and diagnostic uses of antibody specificity profiles
INVENTOR(S):	Robinson, William H., Menlo Park, CA, UNITED STATES Hirschberg, David L., Menlo Park, CA, UNITED STATES Steinman, Lawrence, Palo Alto, CA, UNITED STATES Ruiz, Pedro Jose, Redwood City, CA, UNITED STATES Utz, Paul J., Stanford, CA, UNITED STATES Garren, Hideki, Stanford, CA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003003516	A1	20030102	
APPLICATION INFO.:	US 2002-120578	A1	20020410	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-283090P	20010410	(60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	BOZICEVIC, FIELD & FRANCIS LLP, 200 MIDDLEFIELD RD, SUITE 200, MENLO PARK, CA, 94025
NUMBER OF CLAIMS:	37
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	6 Drawing Page(s)
LINE COUNT:	2167

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides a method for determining the antibody specificity profile in an individual. This specificity profile reveals the individual's immune response to multiple antigens and/or epitopes of autoantigens, allergens, graft antigens, etc. The antibody specificity profile is determined through the binding of patient samples comprising antibodies to the arrays. The array can comprises antigens and epitopes. The invention also provides the means and methods for determining antigen or epitope specificity profiles that can be used in the development of either generic and individualized diagnosis and treatment for immune related diseases, including autoimmune disease, allergy and graft rejection.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L14 ANSWER 2 OF 2 USPATFULL on STN

ACCESSION NUMBER:	2002:191552 USPATFULL
TITLE:	Protein microarrays
INVENTOR(S):	MacBeath, Gavin, Arlington, MA, UNITED STATES Schreiber, Stuart L., Boston, MA, UNITED STATES Sorger, Peter K., Cambridge, MA, UNITED STATES Cardone, Michael H., Boston, MA, UNITED STATES Newman, John, Cambridge, MA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002102617	A1	20020801	
APPLICATION INFO.:	US 2001-923243	A1	20010803	(9)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2000-222709P	20000803	(60)

US 2001-297897P 20010613 (60)
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Timothy J. Oyer, c/o Wolf, Greenfield & Sacks, P.C., Federal Reserve Plaza, 600 Atlantic Avenue, Boston, MA, 02210-2211
NUMBER OF CLAIMS: 105
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 1515
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Driven by the influx of data from genome sequencing projects, systematic efforts are now underway to construct defined sets of cloned genes for high throughput expression and purification of recombinant proteins. To facilitate the subsequent study of protein function, the present invention provides protein microarrays that are compatible with the demand for extremely low sample volume and the rapid, simultaneous processing of thousands of proteins, and methods of assaying these arrays. The proteins are covalently or non-covalently attached to the surface of a solid support and retain their ability to interact specifically with other proteins, polynucleotides, other biological macromolecules, or small molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> file .meeting
'EVENTLINE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files that are available. If you have requested multiple files, you can specify a corrected file name or you can enter "IGNORE" to continue accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	21.36	46.50

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-0.65

FILE 'AGRICOLA' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'BIOTECHNO' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'CONFSCI' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'HEALSAFE' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'IMSDRUGCONF' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'LIFESCI' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'MEDICONF' ENTERED AT 09:49:36 ON 31 JUL 2003

FILE 'PASCAL' ENTERED AT 09:49:36 ON 31 JUL 2003

```
=>  throughput(P)(microarray or screening)(P)(spot or well or dot)
L15           6 FILE AGRICOLA
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
L16         417 FILE BIOTECHNO
L17           2 FILE CONFSCI
L18           0 FILE HEALSAFE
L19           0 FILE IMSDRUGCONF
L20         158 FILE LIFESCI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
L21           0 FILE MEDICONF
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'THROUGHPUT(P)(MICROARRA'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'SCREENING)(P)(SPOT'
L22         266 FILE PASCAL

TOTAL FOR ALL FILES
L23         849 THROUGHPUT(P)(MICROARRAY OR SCREENING)(P)(SPOT OR WELL OR DOT)

=> l23 and (per cm)
L24           0 FILE AGRICOLA
L25           0 FILE BIOTECHNO
L26           0 FILE CONFSCI
L27           0 FILE HEALSAFE
L28           0 FILE IMSDRUGCONF
L29           0 FILE LIFESCI
L30           0 FILE MEDICONF
L31           0 FILE PASCAL

TOTAL FOR ALL FILES
L32           0 L23 AND (PER CM)

=> l23 and per
L33           1 FILE AGRICOLA
L34          33 FILE BIOTECHNO
L35           0 FILE CONFSCI
L36           0 FILE HEALSAFE
L37           0 FILE IMSDRUGCONF
L38          12 FILE LIFESCI
L39           0 FILE MEDICONF
L40          20 FILE PASCAL

TOTAL FOR ALL FILES
L41          66 L23 AND PER

=> l41(L)(per cm)
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L33(L)(PER'
L42           0 FILE AGRICOLA
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L34(L)(PER'
L43           0 FILE BIOTECHNO
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
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FIELD CODE - 'AND' OPERATOR ASSUMED 'L35(L)(PER'
L44           0 FILE CONFSCI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L36(L)(PER'
L45           0 FILE HEALSAFE
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L37(L)(PER'
L46           0 FILE IMSDRUGCONF
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L38(L)(PER'
L47           0 FILE LIFESCI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L39(L)(PER'
L48           0 FILE MEDICONF
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L40(L)(PER'
L49           0 FILE PASCAL

TOTAL FOR ALL FILES
L50           0 L41(L)(PER CM)

=> 141(P)density
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L33(P)DENSITY'
L51           1 FILE AGRICOLA
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L34(P)DENSITY'
L52           5 FILE BIOTECHNO
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L35(P)DENSITY'
L53           0 FILE CONFSCI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L36(P)DENSITY'
L54           0 FILE HEALSAFE
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L37(P)DENSITY'
L55           0 FILE IMSDRUGCONF
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L38(P)DENSITY'
L56           3 FILE LIFESCI
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L39(P)DENSITY'
L57           0 FILE MEDICONF
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L40(P)DENSITY'
L58           2 FILE PASCAL

TOTAL FOR ALL FILES
L59          11 L41(P) DENSITY

=> dup rem
ENTER L# LIST OR (END):159
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF, MEDICONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L59
L60            8 DUP REM L59 (3 DUPLICATES REMOVED)

=> 160 and 1000
L61           1 S L60
L62           0 FILE AGRICOLA
L63           5 S L60
L64           1 FILE BIOTECHNO
L65           0 S L60
L66           0 FILE CONFSCI
```

L67 0 S L60
L68 0 FILE HEALSAFE
L69 0 S L60
L70 0 FILE IMSDRUGCONF
L71 1 S L60
L72 0 FILE LIFESCI
L73 0 S L60
L74 0 FILE MEDICONF
L75 1 S L60
L76 0 FILE PASCAL

TOTAL FOR ALL FILES
L77 1 L60 AND 1000

=> d l77 ibib abs total

L77 ANSWER 1 OF 1 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1997:27371430 BIOTECHNO
TITLE: Proteome research: Complementarity and limitations with respect to the RNA and DNA worlds
AUTHOR: Humphery-Smith I.; Cordwell S.J.; Blackstock W.P.
CORPORATE SOURCE: Dr. I. Humphery-Smith, Centre Proteome Research, National Innovation Centre, Australian Technology Park, Eveleigh, NSW, Australia.
SOURCE: Electrophoresis, (1997), 18/8 (1217-1242), 321 reference(s)
CODEN: ELCTDN ISSN: 0173-0835
DOCUMENT TYPE: Journal; Conference Article
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1997:27371430 BIOTECHNO
AB A methodological overview of proteome analysis is provided along with details of efforts to achieve high-**throughput screening** (HTS) of protein samples derived from two-dimensional electrophoresis gels. For both previously sequenced organisms and those lacking significant DNA sequence information, mass spectrometry has a key role to play in achieving HTS. Prototype robotics designed to conduct appropriate chemistries and deliver 700-**1000** protein (genes) **per** day to batteries of mass spectrometers or liquid chromatography (LC)-based analyses are **well** advanced, as are efforts to produce high **density** gridded arrays containing > **1000** proteins on a single matrix assisted laser desorption ionisation/time-of-flight (MALDI-TOF) sample stage. High sensitivity HTS of proteins is proposed by employing principally mass spectrometry in an hierarchical manner: (i) MALDI-TOF-mass spectrometry (MS) on at least **1000** proteins **per** day; (ii) electrospray ionisation (ESI)/MS/MS for analysis of peptides with respect to predicted fragmentation patterns or by sequence tagging; and (iii) ESI/MS/MS for peptide sequencing. Genomic sequences when complemented with information derived from hybridisation assays and proteome analysis may herald in a new era of holistic cellular biology. The current preoccupation with the absolute quantity of gene-product (RNA and/or protein) should move backstage with respect to more molecularly relevant parameters, such as: molecular half-life; synthesis rate; functional competence (presence or absence of mutations); reaction kinetics; the influence of individual gene-products on biochemical flux; the influence of the environment, cell-cycle, stress and disease on gene-products; and the collective roles of multigenic and epigenetic phenomena governing cellular processes. Proteome analysis is demonstrated as being capable of proceeding independently of DNA sequence information and aiding in genomic annotation. Its ability to confirm the existence of gene-products predicted from DNA sequence is a major contribution to genomic science. The workings of software engines necessary to achieve large-scale

proteome analysis are outlined, along with trends towards miniaturisation, analyte concentration and protein detection independent of staining technologies. A challenge for proteome analysis into the future will be to reduce its dependence on two-dimensional (2-D) gel electrophoresis as the preferred method of separating complex mixtures of cellular proteins. Nonetheless, proteome analysis already represents a means of efficiently complementing differential display, high **density** expression arrays, expressed sequence tags, direct or subtractive hybridisation, chromosomal linkage studies and nucleic acid sequencing as a problem solving tool in molecular biology.

```
=> file .jacob
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       7.93      54.43

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                         ENTRY    SESSION
CA SUBSCRIBER PRICE                                       0.00      -0.65

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FILE 'USPATFULL' ENTERED AT 09:53:17 ON 31 JUL 2003
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=>  throughput(P)(microarray or screening)(P)(spot or well or dot)
L78        1164 FILE CAPLUS
L79         506 FILE BIOSIS
L80         513 FILE MEDLINE
L81         481 FILE EMBASE
L82        4842 FILE USPATFULL

TOTAL FOR ALL FILES
L83        7506 THROUGHPUT(P)(MICROARRAY OR SCREENING)(P)(SPOT OR WELL OR DOT)

=> l83 and (per cm)
L84           0 FILE CAPLUS
L85           0 FILE BIOSIS
L86           0 FILE MEDLINE
L87           0 FILE EMBASE
L88          58 FILE USPATFULL

TOTAL FOR ALL FILES
L89          58 L83 AND (PER CM)

=> l89 and 1000
L90           0 FILE CAPLUS
L91           0 FILE BIOSIS
L92           0 FILE MEDLINE
L93           0 FILE EMBASE
L94          57 FILE USPATFULL
```

```
TOTAL FOR ALL FILES
L95          57 L89 AND 1000

=> l95 and density
L96           0 FILE CAPLUS
L97           0 FILE BIOSIS
L98           0 FILE MEDLINE
L99           0 FILE EMBASE
L100         51 FILE USPATFULL

TOTAL FOR ALL FILES
L101         51 L95 AND DENSITY

=> dup rem
ENTER L# LIST OR (END):l101
PROCESSING COMPLETED FOR L101
L102          51 DUP REM L101 (0 DUPLICATES REMOVED)

=> l102 and (at least)
L103          0 S L102
L104          0 FILE CAPLUS
L105          0 S L102
L106          0 FILE BIOSIS
L107          0 S L102
L108          0 FILE MEDLINE
L109          0 S L102
L110          0 FILE EMBASE
L111         51 S L102
L112         51 FILE USPATFULL

TOTAL FOR ALL FILES
L113         51 L102 AND (AT LEAST)

=> l113 and 1500
L114          0 FILE CAPLUS
L115          0 FILE BIOSIS
L116          0 FILE MEDLINE
L117          0 FILE EMBASE
L118         10 FILE USPATFULL

TOTAL FOR ALL FILES
L119         10 L113 AND 1500

=> d l119 ibib abs total

L119 ANSWER 1 OF 10  USPATFULL on STN
ACCESSION NUMBER:        2003:173923  USPATFULL
TITLE:                   Modulators of bone homeostasis identified in a
                         high-throughput screen
INVENTOR(S):             Rompaey, Luc Van, Keerbergen, BELGIUM
                         Van Es, Helmuth Hendrikus Gerardus, Haarlem,
                         NETHERLANDS
                         Tomme, Peter Herwig Maria, Gent, BELGIUM
                         Klaassen, Hubertus Johannes Matheus, Herent, BELGIUM

                              NUMBER        KIND    DATE
                         ---------------- ------ --------
PATENT INFORMATION:      US 2003119771      A1   20030626
APPLICATION INFO.:       US 2002-225630     A1   20020822  (10)

                                NUMBER         DATE
                         ------------------ --------
PRIORITY INFORMATION:    US 2001-314056P    20010822 (60)
                         US 2002-356935P    20020214 (60)
```

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SYNNESTVEDT & LECHNER, LLP, 2600 ARAMARK TOWER, 1101 MARKET STREET, PHILADELPHIA, PA, 191072950
NUMBER OF CLAIMS: 39
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 25 Drawing Page(s)
LINE COUNT: 4299
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the field of molecular genetics and medicine. In particular, the present invention relates to the field of functional genomics, i.e., to a method for the identification of genes that function in regulating bone homeostasis, such as the induction of osteogenesis.

In particular, the present invention relates to polynucleotides and the encoded polypeptides that are identified in a high-throughput screen designed to detect modulation of bone alkaline phosphatase activity. Moreover, the present invention relates to vectors, host cells, antibodies and diagnostic methods for detecting diseases involving the discovered polynucleotides, and therapeutic methods for treating such diseases. The invention further relates to methods and means for drug compound screens designed to develop new therapeutic strategies.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 2 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:102241 USPATFULL
TITLE: Miniaturized cell array methods and apparatus for cell-based screening
INVENTOR(S): Kapur, Ravi, Gibsonia, PA, United States
Adams, Terri, Pittsburgh, PA, United States
PATENT ASSIGNEE(S): Cellomics, Inc., Pittsburgh, PA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6548263	B1	20030415
APPLICATION INFO.:	US 2000-540862		20000331 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1999-401212, filed on 22 Sep 1999 Continuation-in-part of Ser. No. US 1997-865341, filed on 29 May 1997, now patented, Pat. No. US 6103479

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-138119P	19990607 (60)
	US 1999-127339P	19990401 (60)
	US 1998-101399P	19980922 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Chin, Christopher L.
ASSISTANT EXAMINER: Cook, Lisa V.
LEGAL REPRESENTATIVE: McDonnell Boehnen Hulbert & Berghoff, Harper, David S.
NUMBER OF CLAIMS: 14
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 48 Drawing Figure(s); 48 Drawing Page(s)
LINE COUNT: 3580
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention describes novel methods for making a substrate for selective cell patterning, and the substrates themselves, wherein the method comprises contacting reactive hydroxyl groups on the surface of a substrate with a hydroxyl-reactive bifunctional molecule to form a monolayer, and using stencils to deposit cell repulsive or cell adhesive

moieties in controlled locations on the cell culture substrate. Methods comprising selective differentiation of stem cells to create tissue specific and organ-specific cell substrates, as well as the cell substrates themselves are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 3 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:93021 USPATFULL
TITLE: Anergy-regulated molecules
INVENTOR(S): Rao, Anjana, Cambridge, MA, UNITED STATES
Byrne, Michael, Brookline, MA, UNITED STATES
Macian, Fernando, Quincy, MA, UNITED STATES
PATENT ASSIGNEE(S): The Center For Blood Research, Inc., Boston, MA (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003064380	A1	20030403
APPLICATION INFO.:	US 2002-58024	A1	20020129 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-264876P	20010129 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: FITZPATRICK CELLA HARPER & SCINTO, 30 ROCKEFELLER PLAZA, NEW YORK, NY, 10112
NUMBER OF CLAIMS: 45
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Page(s)
LINE COUNT: 8396
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions for the identification of novel targets for diagnosis, prognosis, therapeutic intervention and prevention of an immune disorder. In particular, the present invention is directed to the identification of novel targets which are anergy markers. The present invention is further directed to methods of high-throughput screening for test compounds capable of modulating the activity of proteins encoded by the novel targets. Moreover, the present invention is also directed to methods that can be used to assess the efficacy of test compounds and therapies for the ability to inhibit an immune disorder. Methods for determining the long term prognosis in a subject are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 4 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:71363 USPATFULL
TITLE: 37 staphylococcus aureus genes and polypeptides
INVENTOR(S): Choi, Gil H., Rockville, MD, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003049648	A1	20030313
APPLICATION INFO.:	US 2002-84205	A1	20020228 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. WO 2000-US23773, filed on 31 Aug 2000, UNKNOWN

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-151933P	19990901 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
NUMBER OF CLAIMS: 21
EXEMPLARY CLAIM: 1
LINE COUNT: 9769
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel genes from S. aureus and the polypeptides they encode. Also provided as are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity. The invention additionally relates to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by Staphylococcus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 5 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:37095 USPATFULL
TITLE: Interface between substrates having microarrays and microtiter plates
INVENTOR(S): MacBeath, Gavin, Arlington, MA, UNITED STATES
Grudzien, Jennipher, Metamora, MI, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003026739	A1	20030206	
APPLICATION INFO.:	US 2002-171128	A1	20020613	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-297991P	20010613	(60)
	US 2001-329253P	20011012	(60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Choate, Hall & Stewart, Exchange Place, 53 State Street, Boston, MA, 02109
NUMBER OF CLAIMS: 135
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 14 Drawing Page(s)
LINE COUNT: 2211
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention describes a process for preparing a microtiter-microarray device that includes a bottomless microtiter plate attached to the first side of one or more substrates with microarrays of materials attached thereto. The microtiter plate and the one or more substrates are attached through one or more gaskets. Preferably, the microtiter plate is attached to one face of the one or more gaskets by an irreversible water-tight seal, and the first side of the one or more substrates is attached to the opposite face of the one or more gaskets by a reversible, water-tight seal.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 6 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2002:312213 USPATFULL
TITLE: Thin-film thermoelectric cooling and heating devices for DNA genomic and proteomic chips, thermo-optical switching circuits, and IR tags
INVENTOR(S): Venkatasubramanian, Rama, Cary, NC, UNITED STATES
PATENT ASSIGNEE(S): Research Triangle Institute, Research Triangle Park, NC, 27709 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002174660	A1	20021128
APPLICATION INFO.:	US 2002-118236	A1	20020409 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-282185P	20010409 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: OBLON SPIVAK MCCLELLAND MAIER & NEUSTADT PC, FOURTH FLOOR, 1755 JEFFERSON DAVIS HIGHWAY, ARLINGTON, VA, 22202
NUMBER OF CLAIMS: 141
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Page(s)
LINE COUNT: 1865

AB A thermoelectric cooling and heating device including a substrate, a plurality of thermoelectric elements arranged on one side of the substrate and configured to perform at **least** one of selective heating and cooling such that each thermoelectric element includes a thermoelectric material, a Peltier contact contacting the thermoelectric material and forming under electrical current flow at **least** one of a heated junction and a cooled junction, and electrodes configured to provide current through the thermoelectric material and the Peltier contact. As such, the thermoelectric cooling and heating device selectively biases the thermoelectric elements to provide on one side of the thermolectric device a grid of localized heated or cooled junctions.

L119 ANSWER 7 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2002:279682 USPATFULL
TITLE: Methods for treating or preventing cardiovascular disorders by modulating metalloprotease function
INVENTOR(S): Chun, Miyoung, Belmont, MA, UNITED STATES
Schonbeck, Uwe, Randolph, MA, UNITED STATES
Libby, Peter, Boston, MA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002155113	A1	20021024
APPLICATION INFO.:	US 2002-97683	A1	20020313 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-275881P	20010313 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: LOUIS MYERS, Fish & Richardson P.C., 225 Franklin Street, Boston, MA, 02110-2804
NUMBER OF CLAIMS: 22
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 3485
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention is based on the finding that human atheroma-associated endothelial cells (EC), smooth muscle cells (SMC) and macrophages express insterstitial collagenase MMP-8 in vitro, as well as in atherosclerotic lesions in situ. Thus, the invention features methods of modulating the activity or expression of MMP-8 and methods of inhibiting collagen degradation, particularly type I collagen degradation. The invention also features methods of treating or preventing non-neutrophil-mediated inflammatory conditions, in

particular cardiovascular disorders such as atherosclerosis; methods of diagnosing and staging such conditions; and methods of evaluating the efficacy of a treatment for such conditions. Finally, the invention features methods of identifying agents that inhibit MMP-8 expression or activity, which can be used for the treatment of non-neutrophil-mediated inflammatory disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 8 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2002:192264 USPATFULL
TITLE: Staphylococcus aureus polynucleotides and polypeptides
INVENTOR(S): Choi, Gil H., Rockville, MD, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002103338	A1	20020801
APPLICATION INFO.:	US 2001-925637	A1	20010810 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. WO 2000-US23773, filed on 31 Aug 2000, UNKNOWN Continuation-in-part of Ser. No. US 1997-781986, filed on 3 Jan 1997, PENDING Continuation-in-part of Ser. No. US 1997-956171, filed on 20 Oct 1997, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-151933P	19990901 (60)
	US 1996-9861P	19960105 (60)
	US 1996-9861P	19960105 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
NUMBER OF CLAIMS: 96
EXEMPLARY CLAIM: 1
LINE COUNT: 9945
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel genes from S. aureus and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity. The invention additionally relates to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by Staphylococcus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 9 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2002:191552 USPATFULL
TITLE: Protein microarrays
INVENTOR(S): MacBeath, Gavin, Arlington, MA, UNITED STATES
Schreiber, Stuart L., Boston, MA, UNITED STATES
Sorger, Peter K., Cambridge, MA, UNITED STATES
Cardone, Michael H., Boston, MA, UNITED STATES
Newman, John, Cambridge, MA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002102617	A1	20020801
APPLICATION INFO.:	US 2001-923243	A1	20010803 (9)

	NUMBER	DATE

PRIORITY INFORMATION:	US 2000-222709P	20000803 (60)
	US 2001-297897P	20010613 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	APPLICATION	
LEGAL REPRESENTATIVE:	Timothy J. Oyer, c/o Wolf, Greenfield & Sacks, P.C., Federal Reserve Plaza, 600 Atlantic Avenue, Boston, MA, 02210-2211	
NUMBER OF CLAIMS:	105	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	13 Drawing Page(s)	
LINE COUNT:	1515	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Driven by the influx of data from genome sequencing projects, systematic efforts are now underway to construct defined sets of cloned genes for high throughput expression and purification of recombinant proteins. To facilitate the subsequent study of protein function, the present invention provides protein microarrays that are compatible with the demand for extremely low sample volume and the rapid, simultaneous processing of thousands of proteins, and methods of assaying these arrays. The proteins are covalently or non-covalently attached to the surface of a solid support and retain their ability to interact specifically with other proteins, polynucleotides, other biological macromolecules, or small molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L119 ANSWER 10 OF 10 USPATFULL on STN

ACCESSION NUMBER:	2000:105664 USPATFULL		
TITLE:	Miniaturized cell array methods and apparatus for cell-based screening		
INVENTOR(S):	Taylor, D. Lansing, Pittsburgh, PA, United States		
PATENT ASSIGNEE(S):	Cellomics, Inc., Pittsburgh, PA, United States (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6103479		20000815
APPLICATION INFO.:	US 1997-865341		19970529 (8)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1997-810983, filed on 27 Feb 1997, now patented, Pat. No. US 5989835		
	NUMBER	DATE	
PRIORITY INFORMATION:	US 1996-18696P	19960530 (60)	
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	Granted		
PRIMARY EXAMINER:	Housel, James C.		
ASSISTANT EXAMINER:	Nguyen, Bao-Thuy L.		
LEGAL REPRESENTATIVE:	McDonnell, Boehnen, Hulbert & Berghoff, Harper, David S.		
NUMBER OF CLAIMS:	5		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	30 Drawing Figure(s); 22 Drawing Page(s)		
LINE COUNT:	1213		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention discloses devices and methods of performing high **throughput screening** of the physiological response of cells to biologically active compounds and methods of combining high-**throughput** with high-content spatial information at the cellular and subcellular level as **well** as temporal information about changes in physiological, biochemical and molecular activities. The present invention allows multiple types of cell interactions to be studied simultaneously by combining multicolor luminescence reading,

microfluidic delivery, and environmental control of living cells in non-uniform micro-patterned arrays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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